

SEQUENCE LISTING

<110> Commonwealth Scientific and Industrial Research Organisation

<120> Expression system

<130> 13447210

<160> 40

<170> PatentIn version 3.2

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<211> 30

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<213> Artificial Sequence

<220>

<223> signal sequence

<400> 1

Met Lys Lys Arg Arg Val Val Asn Ser Val Leu Leu Leu Leu Leu

1 5 10 15

Ala Ser Ala Leu Ala Leu Thr Val Ala Pro Met Ala Lys Ala

20 25 30

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<400> 2

Met Glu Ala Arg Met Thr Gly Arg Arg Lys Val Thr Arg Arg Asp Ala

1 5 10 15

Met Ala Asp Ala Ala Arg Ala Val Gly Val Ala Cys Leu Gly Gly Phe

20 25 30

Ser Leu Ala Ala Leu Val Arg Thr Ala Ser Pro Val Asp Ala

35 40 45

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Met Ser Arg Ser Ala Lys Pro Gln Asn Gly Arg Arg Arg Phe Leu Arg

1 5 10 15

Asp Val Val Arg Thr Ala Gly Gly Leu Ala Ala Val Gly Val Ala Leu

20 25 30

Gly Leu Gln Gln Gln Thr Ala Arg Ala

35 40

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Met Thr Trp Ser Arg Arg Gln Phe Leu Thr Gly Val Gly Val Leu Ala

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Ala Val Ser Gly Thr Ala Gly Arg Val Val Ala

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Ala Thr Val Ala Thr Ala Gly Thr Ala Lys Ala

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Met Ser Glu Lys Asp Lys Met Ile Thr Arg Arg Asp Ala Leu Arg Asn

1 5 10 15
Ile Ala Val Val Val Gly Ser Val Ala Thr Thr Thr Met Met Gly Val
 20 25 30
Gly Val Ala Asp Ala

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Met Gln Ile Val Asn Leu Thr Arg Arg Gly Phe Leu Lys Ala Ala Cys

1 5 10 15
Val Val Thr Gly Gly Ala Leu Ile Ser Ile Arg Met Thr Gly Lys Ala
 20 25 30

Val Ala

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Met Asn Asn Glu Glu Thr Phe Tyr Gln Ala Met Arg Arg Gln Gly Val

1 5 10 15

Thr Arg Arg Ser Phe Leu Lys Tyr Cys Ser Leu Ala Ala Thr Ser Leu

20 25 30

Gly Leu Gly Ala Gly Met Ala Pro Lys Ile Ala Trp Ala

35 40 45

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<400> 9

Met Ser Thr Gly Thr Thr Asn Leu Val Arg Thr Leu Asp Ser Met Asp

1 5 10 15

Phe Leu Lys Met Asp Arg Arg Thr Phe Met Lys Ala Val Ser Ala Leu

20 25 30

Gly Ala Thr Ala Phe Leu Gly Thr Tyr Gln Thr Glu Ile Val Asn Ala

35 40 45

<210> 10

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<400> 10

Met Lys Cys Tyr Ile Gly Arg Gly Lys Asn Gln Val Glu Glu Arg Leu

1

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15

Glu Arg Arg Gly Val Ser Arg Arg Asp Phe Met Lys Phe Cys Thr Ala

20

25

30

Val Ala Val Ala Met Gly Met Gly Pro Ala Phe Ala Pro Lys Val Ala

35

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45

Glu Ala

50

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<400> 11

Met Asn Arg Arg Asn Phe Ile Lys Ala Ala Ser Cys Gly Ala Leu Leu

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15

Thr Gly Ala Leu Pro Ser Val Ser His Ala

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<400> 12

Met Ser His Ala Asp Glu His Ala Gly Asp His Gly Ala Thr Arg Arg

1 5 10 15

Asp Phe Leu Tyr Tyr Ala Thr Ala Gly Ala Gly Thr Val Ala Ala Gly

20 25 30

Ala Ala Ala Trp Thr Leu Val Asn Gln Met Asn Pro

35 40

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<211> 44

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<400> 13

Met Thr Gln Ile Ser Gly Ser Pro Asp Val Pro Asp Leu Gly Arg Arg

1 5 10 15

Gln Phe Met Asn Leu Leu Thr Phe Gly Thr Ile Thr Gly Val Ala Ala

20 25 30

Gly Ala Leu Tyr Pro Ala Val Lys Tyr Leu Ile Pro

35 40

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Met Asp Arg Arg Thr Phe Leu Arg Leu Tyr Leu Leu Val Gly Ala Ala

1 5 10 15

Ile Ala Val Ala Pro Val Ile Lys Pro Ala Leu Asp Tyr Val Gly Tyr

20 25 30

<210> 15

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Met Thr Lys Leu Ser Gly Gln Glu Leu His Ala Glu Leu Ser Arg Arg

1 5 10 15

Ala Phe Leu Ser Tyr Thr Ala Ala Val Gly Ala Leu Gly Leu Cys Gly

20 25 30

Thr Ser Leu Leu Ala Gln Gly Ala Arg Ala

35 40

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<400> 16

Met Thr Leu Thr Arg Arg Glu Phe Ile Lys His Ser Gly Ile Ala Ala

1 5 10 15

Gly Ala Leu Val Val Thr Ser Ala Ala Pro Leu Pro Ala Trp Ala

20 25 30

<210> 17

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Met Thr Ile Ser Arg Arg Asp Leu Leu Lys Ala Gln Ala Ala Gly Ile

1 5 10 15

Ala Ala Met Ala Ala Asn Ile Pro Leu Ser Ser Gln Ala Pro Ala

20 25 30

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Met Ser Glu Ala Leu Ser Gly Arg Gly Asn Asp Arg Arg Lys Phe Leu

1 5 10 15
Lys Met Ser Ala Leu Ala Gly Val Ala Gly Val Ser Gln Ala Val Gly
 20 25 30

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<400> 19

Met Lys Thr Lys Ile Pro Asp Ala Val Leu Ala Ala Glu Val Ser Arg

1 5 10 15
Arg Gly Leu Val Lys Thr Thr Ala Ile Gly Gly Leu Ala Met Ala Ser
 20 25 30

Ser Ala Leu Thr Leu Pro Phe Ser Arg Ile Ala His Ala

35 40 45

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<400> 20

Met Ser Asn Phe Asn Gln Ile Ser Arg Arg Asp Phe Val Lys Ala Ser

1 5 10 15

Ser Ala Gly Ala Ala Leu Ala Val Ser Asn Leu Thr Leu Pro Phe Asn

20

25

30

Val Met Ala

35

<210> 21

<211> 30

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<400> 21

Met Ser Ile Ser Arg Arg Ser Phe Leu Gln Gly Val Gly Ile Gly Cys

1

5

10

15

Ser Ala Cys Ala Leu Gly Ala Phe Pro Pro Gly Ala Leu Ala

20

25

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<210> 22

<211> 37

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<400> 22

Met Lys Thr Val Leu Pro Ser Val Pro Glu Thr Val Arg Leu Ser Arg

1

5

10

15

Arg Gly Phe Leu Val Gln Ala Gly Thr Ile Thr Cys Ser Val Ala Phe

20

25

30

Gly Ser Val Pro Ala

35

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Met Gly Arg Leu Asn Arg Phe Arg Leu Gly Lys Asp Gly Arg Arg Glu

1

5

10

15

Gln Ala Ser Leu Ser Arg Arg Gly Phe Leu Val Thr Ser Leu Gly Ala

20

25

30

Gly Val Met Phe Gly Phe Ala Arg Pro Ser Ser Ala

35

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Met Ser Asp Lys Asp Ser Lys Asn Thr Pro Gln Val Pro Glu Lys Leu

1

5

10

15

Gly Leu Ser Arg Arg Gly Phe Leu Gly Ala Ser Ala Val Thr Gly Ala

20

25

30

Ala Val Ala Ala Thr Ala Leu Gly Gly Ala Val Met Thr Arg Glu Ser

35

40

45

Trp Ala

50

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<400> 25

Met Glu Ser Arg Thr Ser Arg Arg Thr Phe Val Lys Gly Leu Ala Ala

1

5

10

15

Ala Gly Val Leu Gly Gly Leu Gly Leu Trp Arg Ser Pro Ser Trp Ala

20

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30

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<400> 26

Met Ser Leu Ser Arg Arg Gln Phe Ile Gln Ala Ser Gly Ile Ala Leu

1 5 10 15

Cys Ala Gly Ala Val Pro Leu Lys Ala Ser Ala

20

25

<210> 27

<211> 30

<212> PRT

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<400> 27

Met Thr Leu Asn Arg Arg Asp Phe Ile Lys Thr Ser Gly Ala Ala Val

1 5 10 15

Ala Ala Val Gly Ile Leu Gly Phe Pro His Leu Ala Phe Gly

20

25

30

<210> 28

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> signal sequence

<400> 28

Met Thr Asp Ser Arg Ala Asn Arg Ala Asp Ala Thr Arg Gly Val Ala

1 5 10 15

Ser Val Ser Arg Arg Arg Phe Leu Ala Gly Ala Gly Leu Thr Ala Gly

20

25

30

Ala Ile Ala Leu Ser Ser Met Ser Thr Ser Ala Ser Ala

35

40

45

<210> 29

<211> 1155

<212> DNA

<213> Agrobacterium radiobacter

<400> 29

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ggccccattc cagtttcgga agcgggcttc aactgaccc atgagcatat ctgcggcagt	180
tcggcgggat tcctacgtgc gtggccggag tttttcggtg gccgcaaagc tctagcggaa	240
aaggctgtga gaggattacg ccatgccaga tcggctggcg tgcaaaccat cgtcgatgtg	300
tcgactttcg atatcggtcg tgacgtccgt ttattggccg aagtttcgcg ggccgcccgc	360
gtgcatatcg tggcggcgac tggcttatgg ttcgaccgc cactttcaat gcgaatgcgc	420
agcgtcgaag aactgaccca gttcttctcg cgtgaaatcc aacatggcat cgaagacacc	480
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ccagatggaa tggccttcgt ccctctgaga gtgatcccat tcctacgaga gaagggcgtc	1020
ccgccggaaa cgctagcagg cgtaaccgtg gccaatcccg cgcggttctt gtcaccgacc	1080
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gataccgaac gatga

1155

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<213> Agrobacterium radiobacter

<400> 30

Met Gln Thr Arg Arg Asp Ala Leu Lys Ser Ala Ala Ala Ile Thr Leu

1 5 10 15

Leu Gly Gly Leu Ala Gly Cys Ala Ser Met Ala Arg Pro Ile Gly Thr

20 25 30

Gly Asp Leu Ile Asn Thr Val Arg Gly Pro Ile Pro Val Ser Glu Ala

35 40 45

Gly Phe Thr Leu Thr His Glu His Ile Cys Gly Ser Ser Ala Gly Phe

50 55 60

Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg Lys Ala Leu Ala Glu

65 70 75 80

Lys Ala Val Arg Gly Leu Arg His Ala Arg Ser Ala Gly Val Gln Thr

85 90 95

Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg Asp Val Arg Leu Leu

100 105 110

Ala Glu Val Ser Arg Ala Ala Asp Val His Ile Val Ala Ala Thr Gly

115 120 125

Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Met Arg Ser Val Glu Glu

130 135 140

Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln His Gly Ile Glu Asp Thr

145 150 155 160

Gly	Ile	Arg	Ala	Gly	Ile	Ile	Lys	Val	Ala	Thr	Thr	Gly	Lys	Ala	Thr
				165					170					175	
Pro	Phe	Gln	Glu	Leu	Val	Leu	Lys	Ala	Ala	Ala	Arg	Ala	Ser	Leu	Ala
				180					185					190	
Thr	Gly	Val	Pro	Val	Thr	Thr	His	Thr	Ser	Ala	Ser	Gln	Arg	Asp	Gly
				195				200						205	
Glu	Gln	Gln	Ala	Ala	Ile	Phe	Glu	Ser	Glu	Gly	Leu	Ser	Pro	Ser	Arg
				210				215						220	
Val	Cys	Ile	Gly	His	Ser	Asp	Asp	Thr	Asp	Asp	Leu	Ser	Tyr	Leu	Thr
				225				230						235	
Gly	Leu	Ala	Ala	Arg	Gly	Tyr	Leu	Val	Gly	Leu	Asp	Arg	Met	Pro	Tyr
				245					250					255	
Ser	Ala	Ile	Gly	Leu	Glu	Gly	Asn	Ala	Ser	Ala	Leu	Ala	Leu	Phe	Gly
				260					265					270	
Thr	Arg	Ser	Trp	Gln	Thr	Arg	Ala	Leu	Leu	Ile	Lys	Ala	Leu	Ile	Asp
				275					280					285	
Arg	Gly	Tyr	Lys	Asp	Arg	Ile	Leu	Val	Ser	His	Asp	Trp	Leu	Phe	Gly
				290					295					300	
Phe	Ser	Ser	Tyr	Val	Thr	Asn	Ile	Met	Asp	Val	Met	Asp	Arg	Ile	Asn
				305					310					315	
Pro	Asp	Gly	Met	Ala	Phe	Val	Pro	Leu	Arg	Val	Ile	Pro	Phe	Leu	Arg
				325					330					335	
Glu	Lys	Gly	Val	Pro	Pro	Glu	Thr	Leu	Ala	Gly	Val	Thr	Val	Ala	Asn
				340					345					350	
Pro	Ala	Arg	Phe	Leu	Ser	Pro	Thr	Val	Arg	Ala	Val	Val	Thr	Arg	Ser
				355					360					365	
Glu	Thr	Ser	Arg	Pro	Ala	Ala	Pro	Ile	Pro	Arg	Gln	Asp	Thr	Glu	Arg

370

375

380

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<220>

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<400> 31

Met Gln Thr Arg Arg Asp Ala Leu Lys Ser Ala Ala Ala Ile Thr Leu

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10

15

Leu Gly Gly Leu Ala Gly Cys Ala Ser Met Ala Arg

20

25

<210> 32

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> signal sequence

<400> 32

Met Lys Lys Arg Arg Val Val Asn Ser Val Leu Leu Leu Leu Leu Leu

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10

15

Ala Ser Ala Leu Ala Leu Thr Val Ala Pro Met Ala Phe Ala Ala Gly

20

25

30

Ser

<210> 33

<211> 40

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide

<400> 33

gttcagccca tggctaaagc tgcagagcac ggatccgatc

40

<210> 34

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 34

gatcgggatcc gtgctctgca gctttagcca tgggctgaac

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<210> 35

<211> 33

<212> PRT

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<400> 35

Met Lys Lys Arg Arg Val Val Asn Ser Val Leu Leu Leu Leu Leu

1 5 10 15
Ala Ser Ala Leu Ala Leu Thr Val Ala Pro Met Ala Phe Ala Ala Gly
 20 25 30
Ser

<210> 36
<211> 33
<212> PRT
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<400> 36

Met Lys Lys Arg Arg Val Val Asn Ser Val Leu Leu Leu Leu Leu
1 5 10 15
Ala Ser Ala Leu Ala Leu Thr Val Ala Pro Met Ala Lys Ala Ala Glu
 20 25 30
His

<210> 37
<211> 24
<212> DNA
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<220>
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<400> 37

catgtcgaca tggatcccggt cggt

24

<210> 38

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 38

catgaattct tatTTTTtgaa ctggtaa

27

<210> 39

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 39

gtctaaggat ccatgaaaga agaactaaaa acc

33

<210> 40

<211> 30

<212> DNA

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<223> oligonucleotide

<400> 40

gtctaaaagc ttttaccagt ttagctttag